

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

SEQUENCE LISTING

<110> Beraud, Christophe

<120> Novel motor proteins and methods for
their use

<130> 1044

<140> US 09/597,292

<141> 2000-06-20

<150> US 09/295,612

<151> 1999-04-20

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1115

<212> DNA

<213> Human

<400> 1

atgcagccgc gggcggtcg acgcgcaga ggcgcgcga gaigcggca gcttcagcg 60
ggcgatctc aggagctgt cgctgtcgcc taagcaagat tggactact cgctgtccac 120
ctccagctcg ctaggggtg gctgtgcgc tgcggccatt tggatggaa acaggcgag 180
caagtgtatcc cccctgtgtg cggggcatgg acagctgtc tetagagatt gctaactgga 240
ggaaccacca ggagactctc aaataccatgttgcctt ctatggggaggaggactc 300
agcaggacat ctatgcaggat tcagtcgcgc ccatctcaag gcacttgcgt gaaaggcgaga 360
atgcaggatgt gcttcctatggacccacag gagctggaa gacgcacaca atgtggca 420
gcccagacca acctgggtg atccgcggg ctctcatgg cctctgcgc ctcacaagg 480
aggagggtgc cgaggccgg ccatggccgg ttctgtcact catgtttact cttagatct 540
accaggagaa ggatttagac ctccgtggacc ctgttcggg agacctggta atccgagaag 600
actgcgggg gaataatctgtt atccgggtc tctcccaagaa gcccattcgt agctttgcgt 660
attttggcg gcacttcctg ecagccagtc gaaatggac tggatggacc acccggtca 720
accaggcgtc ctcccgcaatgttgc tctgttcaaa ggtggaccag cgggaacgtt 780
tggcccaatt tggccagcga gagggaaaac tctaccgtat tgacttgcgt gggtcagagg 840
acaacccggc cacggcaac aaggcccttc ggtaaaaga gagtgagcc atcaacacet 900
ccctgtttgtt cctggccaaa gttgtatgt cgctgaatca gggcccttctt cgtgtacctt 960
atcgggacag caagctactt cgccttattgc aggactctt ggggtggctca gcccacagta 1020
tccattatgtc caacattgtcc cctgagagac gttctactt agacacagtc tccgcactca 1080
actttgtgc caggtecaag gaggtgtatca attga 1115

<210> 2

<211> 370

<212> PRT

<213> Human

<400> 2

Met Ala Ala Gly Gly Ser Thr Glu Glu Arg Arg Arg Glu Met Ala Ala

1 5 10 15

Ala Ser Ala Ala Ala Ile Ser Gly Ala Gly Arg Cys Arg Leu Ser Lys

20	25	30													
Ile	Gly	Ala	Thr	Arg	Arg	Pro	Pro	Pro	Ala	Arg	Val	Arg	Val	Ala	Val
35	40	45													
Arg	Leu	Arg	Pro	Phe	Val	Asp	Gly	Thr	Ala	Gly	Ala	Ser	Asp	Pro	Pro
50	55	60													
Cys	Val	Arg	Gly	Met	Asp	Ser	Cys	Ser	Leu	Glu	Ile	Ala	Asn	Trp	Arg
65	70	75	80												
Asn	His	Gln	Glu	Thr	Leu	Lys	Tyr	Gln	Phe	Asp	Ala	Phe	Tyr	Gly	Glu
85	90	95													
Arg	Ser	Thr	Gln	Gln	Asp	Ile	Tyr	Ala	Gly	Ser	Val	Gln	Pro	Ile	Leu
100	105	110													
Arg	His	Leu	Leu	Glu	Gly	Gln	Asn	Ala	Ser	Val	Leu	Ala	Tyr	Gly	Pro
115	120	125													
Thr	Gly	Ala	Gly	Lys	Thr	His	Thr	Met	Leu	Gly	Ser	Pro	Glu	Gln	Pro
130	135	140													
Gly	Val	Ile	Pro	Arg	Ala	Leu	Met	Asp	Leu	Leu	Gln	Leu	Thr	Arg	Glu
145	150	155	160												
Glu	Gly	Ala	Glu	Gly	Arg	Pro	Trp	Ala	Leu	Ser	Val	Thr	Met	Ser	Tyr
165	170	175													
Leu	Glu	Ile	Tyr	Gln	Glu	Lys	Val	Leu	Asp	Leu	Leu	Asp	Pro	Ala	Ser
180	185	190													
Gly	Asp	Leu	Val	Ile	Arg	Glu	Asp	Cys	Arg	Gly	Asn	Ile	Leu	Ile	Pro
195	200	205													
Gly	Leu	Ser	Gln	Lys	Pro	Ile	Ser	Ser	Phe	Ala	Asp	Phe	Glu	Arg	His
210	215	220													
Phe	Leu	Pro	Ala	Ser	Arg	Asn	Arg	Thr	Val	Gly	Ala	Thr	Arg	Leu	Asn
225	230	235	240												
Gln	Arg	Ser	Ser	Arg	Ser	His	Ala	Val	Leu	Leu	Val	Lys	Val	Asp	Gln
245	250	255													
Arg	Glu	Arg	Leu	Ala	Pro	Phe	Arg	Gln	Arg	Glu	Gly	Lys	Leu	Tyr	Leu
260	265	270													
Ile	Asp	Leu	Ala	Gly	Ser	Glu	Asp	Asn	Arg	Arg	Thr	Gly	Asn	Lys	Gly
275	280	285													
Leu	Arg	Leu	Lys	Glu	Ser	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Phe	Val	Leu
290	295	300													
Gly	Lys	Val	Val	Asp	Ala	Leu	Asn	Gln	Gly	Leu	Pro	Arg	Val	Pro	Tyr
305	310	315	320												
Arg	Asp	Ser	Lys	Leu	Thr	Arg	Leu	Leu	Gln	Asp	Ser	Leu	Gly	Gly	Ser
325	330	335													
Ala	His	Ser	Ile	Leu	Ile	Ala	Asn	Ile	Ala	Pro	Glu	Arg	Arg	Phe	Tyr
340	345	350													
Leu	Asp	Thr	Val	Ser	Ala	Leu	Asn	Phe	Ala	Ala	Arg	Ser	Lys	Glu	Val
355	360	365													
Ile	Asn														
370															

<210> 3
 <211> 1538
 <212> DNA
 <213> Human

<400> 3
 atgcagccgc gggccggctcg acgcagcaga ggccgcgcgatggccggca gttcagcgg 60
 cggcgatctc aggagctgtt cgttgtccgc taagcaagat tggagctact cgtcgccac 120
 ctcccaagctcg cgtaagggtg gctgtgcac tgcggccatt tggatgatgaa acagcgggag 180

195	200	205													
Pro	Gly	Leu	Ser	Gln	Lys	Pro	Ile	Ser	Ser	Phe	Ala	Asp	Phe	Glu	Arg
210	215	220													
His	Phe	Leu	Pro	Ala	Ser	Arg	Asn	Arg	Thr	Val	Gly	Ala	Thr	Arg	Leu
225	230	235	240												
Asn	Gln	Arg	Ser	Ser	Arg	Ser	His	Ala	Val	Leu	Leu	Val	Val	Asp	
245	250	255													
Gln	Arg	Glu	Arg	Leu	Ala	Pro	Phe	Arg	Gln	Arg	Glu	Gly	Lys	Leu	Tyr
260	265	270													
Leu	Ile	Asp	Leu	Ala	Gly	Ser	Glu	Asp	Asn	Arg	Arg	Thr	Gly	Asn	Lys
275	280	285													
Gly	Leu	Arg	Leu	Lys	Glu	Ser	Gly	Ala	Ile	Asn	Thr	Ser	Leu	Phe	Val
290	295	300													
Leu	Gly	Lys	Val	Val	Asp	Ala	Leu	Asn	Gln	Gly	Leu	Pro	Arg	Val	Pro
305	310	315	320												
Tyr	Arg	Asp	Ser	Lys	Leu	Thr	Arg	Leu	Leu	Gln	Asp	Ser	Leu	Gly	Gly
325	330	335													
Ser	Ala	His	Ser	Ile	Leu	Ile	Ala	Asn	Ile	Ala	Pro	Glu	Arg	Arg	Pha
340	345	350													
Tyr	Leu	Asp	Thr	Val	Ser	Ala	Leu	Asn	Phe	Ala	Ala	Arg	Ser	Lys	Glu
355	360	365													
Val	Ile	Asn	Arg	Pro	Phe	Thr	Asn	Glu	Ser	Leu	Gln	Pro	His	Ala	Leu
370	375	380													
Gly	Pro	Val	Lys	Leu	Ser	Gln	Lys	Glu	Leu	Leu	Gly	Pro	Pro	Glu	Ala
385	390	395	400												
Lys	Arg	Ala	Arg	Gly	Pro	Glu	Glu	Glu	Glu	Ile	Gly	Ser	Pro	Glu	Pro
405	410	415													
Met	Ala	Ala	Pro	Ala	Ser	Ala	Ser	Gln	Lys	Leu	Ser	Pro	Leu	Gln	Lys
420	425	430													
Leu	Ser	Ser	Met	Asp	Pro	Ala	Met	Leu	Glu	Arg	Leu	Leu	Ser	Leu	Asp
435	440	445													
Arg	Leu	Leu	Ala	Ser	Gln	Gly	Ser	Gln	Gly	Ala	Pro	Leu	Leu	Ser	Thr
450	455	460													
Pro	Lys	Arg	Glu	Arg	Met	Val	Leu	Met	Lys	Thr	Val	Glu	Glu	Lys	Asp
465	470	475	480												
Leu	Glu	Ile	Glu	Arg	Leu	Lys	Thr	Lys	Gln	Lys	Glu	Leu	Glu	Ala	Lys
485	490	495													
Met	Leu	Ala	Gln	Lys	Ala	Glu	Glu	Lys	Glu	Asn	His	Cys	Pro	Thr	Met
500	505	510													

<210> 5

<211> 1041

<212> DNA

<213> Human

<400> 5

atgggtcgct	gtccggctaag	caagatttga	gtctactcgtc	gtccacccccc	agcttcgcgtta	60
agggtggctg	tgcgactcgcg	gccattttgt	gatggaaacag	cggggcaag	tgtatcccccc	120
tgtgtgcggg	gcatggacag	ctgcctctcta	gagattgtcta	actggaggaa	ccaccaggag	180
actctcaat	accaggttga	tgcccttctat	ggggagagaga	gtactcagca	ggacatcttat	240
gcagggttcag	tgccatccccat	cctaaaggcac	ttgcgttggaa	ggcagaatgc	cagtgtgttt	300
gcctatggac	ccacaggagc	tgggaagacg	cacacaatgc	ttggcagcccc	agagcaacct	360
gggggtgtatcc	cgcggggctct	catggacccctc	ctgcagctca	caaggggagga	gggttgcggag	420
ggccggccat	gggccttttc	tgccatctatg	tcttacccatg	agatctacca	ggagaaggtt	480
ttagacccctcc	tggaccctgc	ttcgggagac	ctggtaatcc	gagaagactg	ccggggaaat	540

atccgtatc cgggtctctc ccagaagccc atcagtatgtt tgatcggtt tgatcggtt 600
 ttccgtccag ccagtcgaaa tcggactgtt ggagccaccc ggtcaacca ggtctctcc 660
 cgcagtcgtt ctgtgtctt ggatcggtt gaccaggccc aacgtttggc cccatttcg 720
 cagcgagagg gaaaactcta cctgattgtt ttggctgggt cagaggacaa cggcgcaca 780
 ggcaacaagg gcttcggct aaaagagagt ggatcgatca acacccctt gtttgtctg 840
 ggcggaaatgg tagatcgctt gatcgaggc ctccttcgtt tacccatcg ggacaccaag 900
 ctcactcgcc tattcgatca ctcttcgggt ggttcggccc acatgtatcc tattggcaac 960
 attggccctt agagacgtt ctatcgatca acatgtatcc cactcaactt tgatcgccagg 1020
 tccaaaggagg tgatcaattt a 1041

<210> 6
 <211> 346
 <212> PRT
 <213> Human

<400> 6
 Met Gly Arg Cys Arg Leu Ser Lys Ile Gly Ala Thr Arg Arg Pro Pro
 1 5 10 15
 Pro Ala Arg Val Arg Val Ala Val Arg Leu Arg Pro Phe Val Asp Gly
 20 25 30
 Thr Ala Gly Ala Ser Asp Pro Pro Cys Val Arg Gly Met Asp Ser Cys
 35 40 45
 Ser Leu Glu Ile Ala Asn Trp Arg Asn His Gln Glu Thr Leu Lys Tyr
 50 55 60
 Gln Phe Asp Ala Phe Tyr Gly Glu Arg Ser Thr Gln Gln Asp Ile Tyr
 65 70 75 80
 Ala Gly Ser Val Gln Pro Ile Leu Arg His Leu Leu Glu Gly Gln Asn
 85 90 95
 Ala Ser Val Leu Ala Tyr Gly Pro Thr Gly Ala Gly Lys Thr His Thr
 100 105 110
 Met Leu Gly Ser Pro Glu Gln Pro Gly Val Ile Pro Arg Ala Leu Met
 115 120 125
 Asp Leu Leu Gln Leu Thr Arg Glu Glu Gly Ala Glu Gly Arg Pro Trp
 130 135 140
 Ala Leu Ser Val Thr Met Ser Tyr Leu Glu Ile Tyr Gln Glu Lys Val
 145 150 155 160
 Leu Asp Leu Leu Asp Pro Ala Ser Gly Asp Leu Val Ile Arg Glu Asp
 165 170 175
 Cys Arg Gly Asn Ile Leu Ile Pro Gly Leu Ser Gln Lys Pro Ile Ser
 180 185 190
 Ser Phe Ala Asp Phe Glu Arg His Phe Leu Pro Ala Ser Arg Asn Arg
 195 200 205
 Thr Val Gly Ala Thr Arg Leu Asn Gln Arg Ser Ser Arg Ser His Ala
 210 215 220
 Val Leu Leu Val Lys Val Asp Gln Arg Glu Arg Leu Ala Pro Phe Arg
 225 230 235 240
 Gln Arg Glu Gly Lys Leu Tyr Leu Ile Asp Leu Ala Gly Ser Glu Asp
 245 250 255
 Asn Arg Arg Thr Gly Asn Lys Gly Leu Arg Leu Lys Glu Ser Gly Ala
 260 265 270
 Ile Asn Thr Ser Leu Phe Val Leu Gly Lys Val Val Asp Ala Leu Asn
 275 280 285
 Gln Gly Leu Pro Arg Val Pro Tyr Arg Asp Ser Lys Leu Thr Arg Leu
 290 295 300
 Leu Gln Asp Ser Leu Gly Gly Ser Ala His Ser Ile Leu Ile Ala Asn

305 310 315 320
 Ile Ala Pro Glu Arg Arg Phe Tyr Leu Asp Thr Val Ser Ala Leu As
 325 330 335
 Phe Ala Ala Arg Ser Lys Glu Val Ile Asn
 340 345

<210> 7
<211> 1464
<212> DNA
<213> Human

<400> 7

atgggtcgct	gtccggtaa	caagatgg	gtactcg	gtccaccc	tc	agtcgcgt	60
agggtggctg	tgccgact	gcgcatttg	gtggaa	cagg	ggc	tgatcccc	120
tgtgtgggg	gcatgg	acag	ctgc	tc	ta	actggaggaa	180
acttc	aaat	accagg	tttg	tgcc	ttat	ggggagagga	240
gcagggttc	cag	tgcc	gccc	at	ct	gtactcg	300
gcttatgg	ac	ccac	agg	gg	aa	atgc	360
gggggtatcc	cg	gggg	ct	at	tg	caatgc	420
ggcggccat	gg	gg	cc	tt	tc	tttac	480
tttagac	tt	gg	ac	cc	tc	tttac	540
atccgtatcc	tt	gg	ac	cc	tc	tttac	600
ttccgtccag	cc	ag	tt	cc	at	tttac	660
cgcagt	tc	at	gt	tc	cc	tttgc	720
cagc	gag	agg	aa	ac	tc	tttgc	780
ggcaacaagg	gc	ctt	cg	gt	aa	ag	840
ggcaaa	ag	ttt	gg	ttt	ttt	tttgc	900
ctcactcgcc	tat	tc	gg	ttt	ttt	tttgc	960
attggccc	ttt	ttt	ttt	ttt	ttt	tttgc	1020
tccaggagg	tg	at	ca	at	cc	tttgc	1080
cctgtta	ag	tc	tc	tc	tc	tttgc	1140
cctg	agg	agg	at	ttt	ttt	tttgc	1200
aaactc	cag	cc	c	tc	tc	tttgc	1260
agcttgg	gac	tc	tc	tc	tc	tttgc	1320
aagc	gag	g	tg	ttt	ttt	tttgc	1380
ctt	aa	gg	at	ttt	ttt	tttgc	1440
gagaaccatt	gt	cc	ca	at	tt	tttgc	1464

<210> 8
<211> 487
<212> PRT
<213> Human

<400> 8
 Met Gly Arg Cys Arg Leu Ser Lys Ile Gly Ala Thr Arg Arg Pro Pro
 1 5 10 15
 Pro Ala Arg Val Arg Val Ala Val Arg Leu Arg Pro Phe Val Asp Gly
 20 25 30
 Thr Ala Gly Ala Ser Asp Pro Pro Cys Val Arg Gly Met Asp Ser Cys
 35 40 45
 Ser Leu Glu Ile Ala Asn Trp Arg Asn His Glu Glu Thr Leu Lys Tyr
 50 55 60
 Gln Phe Asp Ala Phe Tyr Gly Glu Arg Ser Thr Gln Gln Asp Ile Tyr
 65 70 75 80
 Ala Gly Ser Val Gin Pro Ile Leu Arg His Leu Leu Glu Gly Gin Asn

85	90	95	
Ala Ser Val Leu Ala Tyr Gly Pro Thr Gly Ala Gly Lys Thr His Thr			
100	105	110	
Met Leu Gly Ser Pro Glu Gln Pro Gly Val Ile Pro Arg Ala Leu Met			
115	120	125	
Asp Leu Leu Gln Leu Thr Arg Glu Glu Gly Ala Glu Gly Arg Pro Trp			
130	135	140	
Ala Leu Ser Val Thr Met Ser Tyr Leu Glu Ile Tyr Gln Glu Lys Val			
145	150	155	160
Leu Asp Leu Leu Asp Pro Ala Ser Gly Asp Leu Val Ile Arg Glu Asp			
165	170	175	
Cys Arg Gly Asn Ile Leu Ile Pro Gly Leu Ser Gln Lys Pro Ile Ser			
180	185	190	
Ser Phe Ala Asp Phe Glu Arg His Phe Leu Pro Ala Ser Arg Asn Arg			
195	200	205	
Thr Val Gly Ala Thr Arg Leu Asn Gln Arg Ser Ser Arg Ser His Ala			
210	215	220	
Val Leu Leu Val Lys Val Asp Gln Arg Glu Arg Leu Ala Pro Phe Arg			
225	230	235	240
Gln Arg Glu Gly Lys Leu Tyr Leu Ile Asp Leu Ala Gly Ser Glu Asp			
245	250	255	
Asn Arg Arg Thr Gly Asn Lys Gly Leu Arg Leu Lys Glu Ser Gly Ala			
260	265	270	
Ile Asn Thr Ser Leu Phe Val Leu Gly Lys Val Val Asp Ala Leu Asn			
275	280	285	
Gln Gly Leu Pro Arg Val Pro Tyr Arg Asp Ser Lys Leu Thr Arg Leu			
290	295	300	
Leu Gln Asp Ser Leu Gly Gly Ser Ala His Ser Ile Leu Ile Ala Asn			
305	310	315	320
Ile Ala Pro Glu Arg Arg Phe Tyr Leu Asp Thr Val Ser Ala Leu Asn			
325	330	335	
Phe Ala Ala Arg Ser Lys Glu Val Ile Asn Arg Pro Phe Thr Asn Glu			
340	345	350	
Ser Leu Gln Pro His Ala Leu Gly Pro Val Lys Leu Ser Gln Lys Glu			
355	360	365	
Leu Leu Gly Pro Pro Glu Ala Lys Arg Ala Arg Gly Pro Glu Glu Glu			
370	375	380	
Glu Ile Gly Ser Pro Glu Pro Met Ala Ala Pro Ala Ser Ala Ser Gln			
385	390	395	400
Lys Leu Ser Pro Leu Gln Lys Leu Ser Ser Met Asp Pro Ala Met Leu			
405	410	415	
Glu Arg Leu Leu Ser Leu Asp Arg Leu Leu Ala Ser Gln Gly Ser Gln			
420	425	430	
Gly Ala Pro Leu Leu Ser Thr Pro Lys Arg Glu Arg Met Val Leu Met			
435	440	445	
Lys Thr Val Glu Glu Lys Asp Leu Glu Ile Glu Arg Leu Lys Thr Lys			
450	455	460	
Gln Lys Glu Leu Glu Ala Lys Met Leu Ala Gln Lys Ala Glu Glu Lys			
465	470	475	480
Glu Asn His Cys Pro Thr Met			
485			